

RAW SEQUENCE LISTING

DATE: 08/06/2001

PATENT APPLICATION: US/09/917,265

TIME: 15:33:39

Input Set : A:\IM-5.txt

Output Set: N:\CRF3\08062001\I917265.raw

```

70 Thr Ile Ser Val Asn Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu Asn
71      100      105      110
W--> 73 aaa att att tcc ttt aa~ gga atg agt cct cct gag agt atc aat gat      500
W--> 74 Lys Ile Ile Ser Phe Xaa Gly Met Ser Pro Pro Glu Ser Ile Asn Asp
75      115      120      125
77 gaa gga aat gac at      514
78 Glu Gly Asn Asp
79 130
82 <210> SEQ ID NO: 2
83 <211> LENGTH: 133
84 <212> TYPE: PRT
85 <213> ORGANISM: Felis catus
87 <220> FEATURE:
88 <221> NAME/KEY: misc_feature
89 <222> LOCATION: (119)..(119)
90 <223> OTHER INFORMATION: The 'Xaa' at location 119 stands for Lys, or Asn.
92 <220> FEATURE:
93 <221> NAME/KEY: misc_feature
94 <222> LOCATION: (470)..(470)
95 <223> OTHER INFORMATION: n = unknown at position 470
96      Xaa = unknown at position 119
98 <400> SEQUENCE: 2
100 Met Thr Ala Ile Pro Val Asp Asp Cys Ile Asn Phe Val Gly Met Lys
101 1      5      10      15
104 Phe Ile Asp Asn Thr Leu Tyr Phe Val Ala Asp Ser Asp Glu Asn Leu
105      20      25      30
108 Glu Thr Asp Tyr Phe Gly Lys Leu Glu His Lys Leu Ser Ile Leu Arg
109      35      40      45
112 Asn Leu Asn Asp Gln Val Leu Phe Ile Asn Gln Gly Asp Gln Pro Val
113      50      55      60
116 Phe Glu Asp Met Pro Asp Ser Asp Cys Thr Asp Asn Ala Pro Arg Thr
117 65      70      75      80
120 Glu Phe Ile Ile Tyr Met Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala
121      85      90      95
124 Val Thr Ile Ser Val Asn Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu
125      100      105      110
W--> 128 Asn Lys Ile Ile Ser Phe Xaa Gly Met Ser Pro Pro Glu Ser Ile Asn
129      115      120      125
132 Asp Glu Gly Asn Asp
133      130
136 <210> SEQ ID NO: 3
137 <211> LENGTH: 514
138 <212> TYPE: DNA
139 <213> ORGANISM: Felis catus
141 <220> FEATURE:
142 <221> NAME/KEY: misc_feature
143 <222> LOCATION: (45)..(45)
144 <223> OTHER INFORMATION: n = unknown at position 45
147 <400> SEQUENCE: 3

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```

W--> 148 atgtcatttc cttcatcatt gatactctca ggaggactca ttccnttaaa ggaaataatt      60
150 ttgttctcac aggagagagt agacatggtc ttataattca cagagatggt tactgccaga      120
152 cctctagtga ggctatcttt atacatatat atgataaatt cagtccgggg tgcattatct      180
154 gtacagtcag aatcaggcat atcctcaaac acaggttgat ctccctgggt aatgaagaga      240
156 acttggtcgt tcaagtttcg taagattgag agtttatggt caagcttgcc aaagtaatct      300
158 gtttccaggt tttcatcact gtcagctaca aagtaaagtg tattgtcaat aaatttcatt      360
160 cccacaaaagt tgatgcaatc atctactggg atagcagtca tctttatccc tgtgctcaat      420
162 agtttcctaa gagaggaagg gatctggaag gtttgaggtc cctttctttt cctgagctgt      480
164 gtagatggca gaaggtggca ggagcgcctt tagc      514
167 <210> SEQ ID NO: 4
168 <211> LENGTH: 502
169 <212> TYPE: DNA
170 <213> ORGANISM: Felis catus
172 <220> FEATURE:
173 <221> NAME/KEY: CDS
174 <222> LOCATION: (3)..(464)
175 <223> OTHER INFORMATION:
178 <220> FEATURE:
179 <221> NAME/KEY: misc_feature
180 <222> LOCATION: (126)..(126)
181 <223> OTHER INFORMATION: n = unknown at position 126
182     Xaa = unknown at position 43
185 <400> SEQUENCE: 4
186 gc aag ctt gaa cat aaa ctc tca atc tta cga aac ttg aac gac caa      47
187   Lys Leu Glu His Lys Leu Ser Ile Leu Arg Asn Leu Asn Asp Gln
188     1             5             10             15
190 gtt ctc ttc att aac cag gga gat caa cct gtg ttt gag gat atg cct      95
191 Val Leu Phe Ile Asn Gln Gly Asp Gln Pro Val Phe Glu Asp Met Pro
192             20             25             30
W--> 194 gat tct gac tgt aca gat aat gca ccc cgg nct gaa ttt atc ata tat      143
W--> 195 Asp Ser Asp Cys Thr Asp Asn Ala Pro Arg Xaa Glu Phe Ile Ile Tyr
196             35             40             45
198 atg tat aaa gat agc ctc act aga ggt ctg gca gta acc atc tct gtg      191
199 Met Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala Val Thr Ile Ser Val
200             50             55             60
202 aat tat aag acc atg tct act ctc tcc tgt gag aac aaa att att tcc      239
203 Asn Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu Asn Lys Ile Ile Ser
204             65             70             75
206 ttt aag gaa atg agt cct cct gag agt atc aat gat gaa gga aat gac      287
207 Phe Lys Glu Met Ser Pro Glu Ser Ile Asn Asp Glu Gly Asn Asp
208 80             85             90             95
210 atc ata ttc ttt cag aga agt gtt cca gga cat gat gat aag ata caa      335
211 Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asp Lys Ile Gln
212             100            105            110
214 ttt gag tct tca ttg tac aag ggg tac ttt cta gct tgt gaa aaa gag      383
215 Phe Glu Ser Ser Leu Tyr Lys Gly Tyr Phe Leu Ala Cys Glu Lys Glu
216             115            120            125
218 aaa gat ctt ttc aaa ctc att ttg aaa aaa aag gat gaa aat ggg gat      431
219 Lys Asp Leu Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu Asn Gly Asp

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```

220          130          135          140
222 aag tcc ata atg ttc act gtt caa aac aag aat tagatattaa aattgcataa      484
223 Lys Ser Ile Met Phe Thr Val Gln Asn Lys Asn
224          145          150
226 tttgaaaaaa aaaaaaaa      502
229 <210> SEQ ID NO: 5
230 <211> LENGTH: 154
231 <212> TYPE: PRT
232 <213> ORGANISM: Felis catus
234 <220> FEATURE:
235 <221> NAME/KEY: misc_feature
236 <222> LOCATION: (42)..(42)
237 <223> OTHER INFORMATION: The 'Xaa' at location 42 stands for Thr, Ala, Pro, or Ser.
239 <220> FEATURE:
240 <221> NAME/KEY: misc_feature
241 <222> LOCATION: (126)..(126)
242 <223> OTHER INFORMATION: n = unknown at position 126
243 Xaa = unknown at position 43
245 <400> SEQUENCE: 5
247 Lys Leu Glu His Lys Leu Ser Ile Leu Arg Asn Leu Asn Asp Gln Val
248 1          5          10          15
251 Leu Phe Ile Asn Gln Gly Asp Gln Pro Val Phe Glu Asp Met Pro Asp
252          20          25          30
W--> 255 Ser Asp Cys Thr Asp Asn Ala Pro Arg Xaa Glu Phe Ile Ile Tyr Met
256          35          40          45
259 Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala Val Thr Ile Ser Val Asn
260          50          55          60
263 Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu Asn Lys Ile Ile Ser Phe
264 65          70          75          80
267 Lys Glu Met Ser Pro Pro Glu Ser Ile Asn Asp Glu Gly Asn Asp Ile
268          85          90          95
271 Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asp Lys Ile Gln Phe
272          100          105          110
275 Glu Ser Ser Leu Tyr Lys Gly Tyr Phe Leu Ala Cys Glu Lys Glu Lys
276          115          120          125
279 Asp Leu Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu Asn Gly Asp Lys
280          130          135          140
283 Ser Ile Met Phe Thr Val Gln Asn Lys Asn
284 145          150
287 <210> SEQ ID NO: 6
288 <211> LENGTH: 502
289 <212> TYPE: DNA
290 <213> ORGANISM: Felis catus
292 <220> FEATURE:
293 <221> NAME/KEY: misc_feature
294 <222> LOCATION: (377)..(377)
295 <223> OTHER INFORMATION: n = unknown at position 377
298 <400> SEQUENCE: 6
299 tttttttttt ttttcaaatt atgcaatttt aatatctaatt tcttgttttg aacagtgaac      60

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```

301 attatggact tatccccatt ttcattccttt tttttcaaaa tgagtttgaa aagatctttc 120
303 tctttttcac aagctagaaa gtaccccttg tacaatgaag actcaaattg tatcttatca 180
305 tcatgtcctg gaacacttct ctgaaagaat atgatgtcat ttccttcacg attgatactc 240
307 tcaggaggac tcatttcctt aaaggaaata attttgttct cacaggagag agtagacatg 300
309 gtcttataat tcacagagat ggttactgcc agacctctag tgaggctatc tttatacata 360
W--> 311 tatatgataa attcagñccg ggggtgcatta tctgtacagt cagaatcagg catatcctca 420
313 aacacaggtt gatctccctg gttaatgaag agaacttggc cgttcaagtt tcgtaagatt 480
315 gagagtttat gttcaagctt gc 502
318 <210> SEQ ID NO: 7
319 <211> LENGTH: 607
320 <212> TYPE: DNA
321 <213> ORGANISM: Felis catus
323 <220> FEATURE:
324 <221> NAME/KEY: CDS O✓
325 <222> LOCATION: (24)..(599)
326 <223> OTHER INFORMATION:
329 <400> SEQUENCE: 7
330 aactattgag cacagggata aag atg act gct ata cca gta gat gat tgc atc 53
331 Met Thr Ala Ile Pro Val Asp Asp Cys Ile
332 1 5 10
334 aac ttt gtg gga atg aaa ttt att gac aat aca ctt tac ttt gta gct 101
335 Asn Phe Val Gly Met Lys Phe Ile Asp Asn Thr Leu Tyr Phe Val Ala
336 15 20 25
338 gac agt gat gaa aac ctg gaa aca gat tac ttt ggc aag ctt gaa cat 149
339 Asp Ser Asp Glu Asn Leu Glu Thr Asp Tyr Phe Gly Lys Leu Glu His
340 30 35 40
342 aaa ctc tca atc tta cga aac ttg aac gac caa gtt ctc ttc att aac 197
343 Lys Leu Ser Ile Leu Arg Asn Leu Asn Asp Gln Val Leu Phe Ile Asn
344 45 50 55
346 cag gga gat caa cct gtg ttt gag gat atg cct gat tct gac tgt aca 245
347 Gln Gly Asp Gln Pro Val Phe Glu Asp Met Pro Asp Ser Asp Cys Thr
348 60 65 70
350 gat aat gca ccc cgg act gaa ttt atc ata tat atg tat aaa gat agc 293
351 Asp Asn Ala Pro Arg Thr Glu Phe Ile Ile Tyr Met Tyr Lys Asp Ser
352 75 80 85 90
354 ctc act aga ggt ctg gca gta acc atc tct gtg aat tat aag acc atg 341
355 Leu Thr Arg Gly Leu Ala Val Thr Ile Ser Val Asn Tyr Lys Thr Met
356 95 100 105
358 tct act ctc tcc tgt gag aac aaa att att tcc ttt aag gaa atg agt 389
359 Ser Thr Leu Ser Cys Glu Asn Lys Ile Ile Ser Phe Lys Glu Met Ser
360 110 115 120
362 cct cct gag agt atc aat gat gaa gga aat gac atc ata ttc ttt cag 437
363 Pro Pro Glu Ser Ile Asn Asp Glu Gly Asn Asp Ile Ile Phe Phe Gln
364 125 130 135
366 aga agt gtt cca gga cat gat gat aag ata caa ttt gag tct tca ttg 485
367 Arg Ser Val Pro Gly His Asp Asp Lys Ile Gln Phe Glu Ser Ser Leu
368 140 145 150
370 tac aag ggg tac ttt cta gct tgt gaa aaa gag aaa gat ctt ttc aaa 533
371 Tyr Lys Gly Tyr Phe Leu Ala Cys Glu Lys Glu Lys Asp Leu Phe Lys

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

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Input Set : A:\IM-5.txt

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L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:73 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:74 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:128 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:148 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:194 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:195 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:255 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:311 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:1079 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:1138 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2582 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (42) SEQUENCE:
L:4269 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (64) SEQUENCE:
L:4277 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (65) SEQUENCE: